



## SEQUENCE LISTING

<110> Arkowitz, Robert A  
Nern, Peter MA

&lt;120&gt; NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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<140> 10/054399

<141> 2002-01-21

<150> 09/168,474

<151> 1998-10-08

<150> 08/951,141

<151> 1997-10-15

<150> 09/529,106

<151> 2000-04-07

<150> US 09/732,180

<151> 2000-12-07

<150> US 60/169,699

<151> 1999-12-07

<150> PCT/GB98/03033

<151> 1998-10-08

<150> 9812793.9

<151> 1998-06-12

<150> 9721357.3

<151> 1997-10-08

<150> 9721358.1

<151> 1997-10-08

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&lt;170&gt; PatentIn Ver. 2.0

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&lt;212&gt; DNA

<213> Saccharomyces cerevisiae

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$\langle 223 \rangle$

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tttgatttta  acgatgagga  gcttttcact  atatccgacg  tttttgccaa  ctcgacgtcc  180
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<212> PRT

<213> Saccharomyces cerevisiae

<220>

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1 5 10 15

Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp  
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu  
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys  
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Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser  
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: nucleic acid

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tttgacttta acgatgagga gcttttcact atatccgacg tttttgccaa ctgcacgtcc 180  
cagctggtca aagtgctaga agtagtagaa acgctaata attccagc 228

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<223> Description of Artificial Sequence: amino acid

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Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro  
1 5 10 15

Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp  
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu  
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys  
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser  
65 70 75

<210> 5

<211> 228

<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: nucleic acid

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tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180  
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<223> Description of Artificial Sequence: amino acid

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1 5 10 15  
Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp  
20 25 30  
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu  
35 40 45  
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys  
50 55 60  
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser  
65 70 75

<210> 7  
<211> 228  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: nucleic acid

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tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180  
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<210> 8  
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<223> Description of Artificial Sequence: amino acid

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Val Ile Ala Pro Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp	20	25	30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu	35	40	45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys	50	55	60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser	65	70	75

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Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala
35 40 45
Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu
50 55 60
Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys
65 70 75 80
His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala
85 90 95
Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser
100 105 110
Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr
115 120 125
Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu
130 135 140
Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala
145 150 155 160
Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg
165 170 175
Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val
180 185 190
Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe

195 200 205

Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg  
210 215 220

Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu  
225 230 235 240

Val Val Thr Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser  
245 250 255

Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly  
260 265 270

Ser Pro His His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Ser  
275 280 285

Asn Asn Ile His Leu Ser Ser Ser Ser Ala Ala Ala Ile Ile His Ser  
290 295 300

Ser Thr Asn Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser  
305 310 315 320

Leu Phe Lys Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg  
325 330 335

Ile Met Ile Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser  
340 345 350

Leu Asn Ile Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu  
355 360 365

Lys Phe Lys Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln  
370 375 380

Gln Leu Ile His Asp Leu Lys Asn  
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<210> 10  
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<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<223>

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gccagacaag agagtaaaca gttcatgct caaataaata aagcaaaaca caagatacaa 180  
gatgcaagct tattccagat ggccaacaaa gttacttcgt tgaccaaaaa taagatcaac 240  
ttaaagccaa atatcgtggt gaaaggccat aataataaaa tctcagattt tcgggtggagt 300  
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atttcgcat cgagtacttt ggtagcaagc gcaggattaa acaataactg taccatttat 480  
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ttaggatgat ttttggcatt agctattcct gaagagccaa acttagaaaa ttcttcgaac 720  
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Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn  
 225 230 235 240  
 Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser  
 245 250 255  
 Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile  
 260 265 270  
 Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser  
 275 280 285  
 Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile  
 290 295 300  
 Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro  
 305 310 315 320  
 Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln  
 325 330 335  
 Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val  
 340 345 350  
 Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr  
 355 360 365  
 Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly  
 370 375 380  
 Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro  
 385 390 395 400  
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 Trp Ser Pro Gly Tyr Gln  
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<210> 12

<211> 1269

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid

<400> 12

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gatgcaagct	tattccagat	ggccaacaaa	gttacttcgt	tgaccaaaaa	taagatcaac	240
ttaaagccaa	atatcgtgtt	gaaaggccat	aataataaaa	tctcagattt	tcggtggagt	300
cgagattcaa	aacgtatatt	gagtgcgaag	caagatggct	ttatgcttat	atgggacagt	360
gcttcagggt	taaaacagaa	cgctattcca	ttagattctc	aatgggttct	ttcctgcgct	420
atttcgcat	cgagtacttt	ggtagcaagc	gcaggattaa	acaataactg	taccatttat	480
agagtttcga	aagaaaacag	agtagcgcaa	aacgttgcgt	caattttcaa	aggacatact	540
tgctatattt	ctgacattga	atttacagat	aacgcacata	tattgacagc	aagtgggggat	600
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<210> 13

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid sequence

<400> 13

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			20					25					30		

Glu	Ile	Gln	Asn	Lys	Ile	Glu	Ala	Ala	Arg	Gln	Glu	Ser	Lys	Gln	Leu
		35					40					45			

His	Ala	Gln	Ile	Asn	Lys	Ala	Lys	His	Lys	Ile	Gln	Asp	Ala	Ser	Leu
	50					55					60				

Phe	Gln	Met	Ala	Asn	Lys	Val	Thr	Ser	Leu	Thr	Lys	Asn	Lys	Ile	Asn
65					70					75					80

Leu	Lys	Pro	Asn	Ile	Val	Leu	Lys	Gly	His	Asn	Asn	Lys	Ile	Ser	Asp
			85						90					95	

Phe	Arg	Trp	Ser	Arg	Asp	Ser	Lys	Arg	Ile	Leu	Ser	Ala	Ser	Gln	Asp
			100					105						110	

Gly	Phe	Met	Leu	Ile	Trp	Asp	Ser	Ala	Ser	Gly	Leu	Lys	Gln	Asn	Ala
		115				120						125			

Ile	Pro	Leu	Asp	Ser	Gln	Trp	Val	Leu	Ser	Cys	Ala	Ile	Ser	Pro	Ser
	130					135					140				

Ser	Thr	Leu	Val	Ala	Ser	Ala	Gly	Leu	Asn	Asn	Asn	Cys	Thr	Ile	Tyr
145					150					155					160

Arg	Val	Ser	Lys	Glu	Asn	Arg	Val	Ala	Gln	Asn	Val	Ala	Ser	Ile	Phe
			165						170					175	

Lys	Gly	His	Thr	Cys	Tyr	Ile	Ser	Asp	Ile	Glu	Phe	Thr	Asp	Asn	Ala
		180						185					190		

His	Ile	Leu	Thr	Ala	Ser	Gly	Asp	Met	Thr	Cys	Ala	Leu	Trp	Asp	Ile
		195					200						205		

Pro	Lys	Ala	Lys	Arg	Val	Arg	Gly	Tyr	Ser	Asp	His	Leu	Gly	Asp	Val
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210 215 220

Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn  
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Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser  
 245 250 255

Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile  
 260 265 270

Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser  
 275 280 285

Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile  
 290 295 300

Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro  
 305 310 315 320

Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln  
 325 330 335

Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val  
 340 345 350

Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr  
 355 360 365

Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly  
 370 375 380

Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro  
 385 390 395 400

Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile  
 405 410 415

Trp Ser Pro Gly Tyr Gln  
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<210> 14  
 <211> 1269  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: nucleic acid  
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 atttcgccat cgagtacttt ggtagcaagc gcaggattaa acaataactg taccatttat 480  
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1269

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<210> 15

<211> 422

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: amino acid sequence

<400> 15

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Met Ala His Gln Met Asp Ser Ile Thr Tyr Ser Asn Asn Val Thr Gln
  1              5              10              15

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Gln Tyr Ile Gln Pro Gln Ser Leu Gln Asp Ile Ser Ala Val Glu Glu
      20              25              30

```

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Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
    35              40              45

```

```

His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
    50              55              60

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```

Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
    65              70              75              80

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```

Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
      85              90              95

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```

Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
    100              105              110

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Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
    115              120              125

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Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
    130              135              140

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Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
    145              150              155              160

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Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
    165              170              175

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Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
    180              185              190

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His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile

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195	200	205
Pro Lys Ala Lys Arg Val Arg Glu Tyr Ser Asp His Leu Gly Asp Val		
210	215	220
Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn		
225	230	235 240
Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser		
	245	250 255
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile		
	260	265 270
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser		
	275	280 285
Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile		
	290	300
Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro		
305	310	315 320
Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln		
	325	330 335
Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Ala Val		
	340	345 350
Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr		
	355	360 365
Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly		
	370	375 380
Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro		
385	390	395 400
Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile		
	405	410 415
Trp Ser Pro Gly Tyr Gln		
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<210> 16

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid  
sequence

<400> 16

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

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5

<210> 17

<211> 7

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid  
sequence

<400> 17  
Gln Asn Leu Tyr Phe Gln Gly  
1 5

<210> 18  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid  
sequence

<400> 18  
Gln Phe Lys Leu Pro Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys  
1 5 10 15

Lys Ser Ile

<210> 19  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid  
sequence

<400> 19  
Gln Phe Lys Leu Pro Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys  
1 5 10 15

Lys Ser Ile

<210> 20  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: amino acid  
sequence

<400> 20  
Gln Phe Lys Leu Pro Val Ile Ala Pro Asp Asp Leu Lys Val Cys Lys  
1 5 10 15

Lys Ser Ile

<210> 21

<211> 19  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<220>  
<223>

<400> 21  
Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys  
1 5 10 15

Lys Ser Ile

<210> 22  
<211> 19  
<212> PRT  
<213> Human

<220>  
<223>

<400> 22  
Gln Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met  
1 5 10 15

Lys Thr Ile

<210> 23  
<211> 2535  
<212> DNA  
<213> *Candida albicans*

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ttcaataaac caagtactcc caaagaccat ttattctatc gatgtgaatc actaaaacga 180  
aaactacaaa aaatccctgg catggaacca tttttgaacc aagctttcaa tcaggctgaa 240  
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agtaatggca aacgtcatca atcattagac ggtgccatga atagactttc agttggttct 360  
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gaggcgcaaa gacgagcaga aaatatcgaa catttggaag aactaaaaga aagagtaggt 1440  
aattggcgtg ggtttaattt ggatgctcaa ggagaactat tattccacgg acaagttggg 1500

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<210> 24  
 <211> 844  
 <212> PRT  
 <213> Candida albicans

<400> 24

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Ser	Ser	Leu	Asn	Ser	Val	Ser	Thr	Val	Ser	Ser	Ser	Arg	Ile	Val	Ser	20	25	30	
Ser	Gly	Pro	Val	Asn	Ile	Asn	Asn	Phe	Asn	Lys	Pro	Ser	Thr	Pro	Lys	35	40	45	
Asp	His	Leu	Phe	Tyr	Arg	Cys	Glu	Ser	Leu	Lys	Arg	Lys	Leu	Gln	Lys	50	55	60	
Ile	Pro	Gly	Met	Glu	Pro	Phe	Leu	Asn	Gln	Ala	Phe	Asn	Gln	Ala	Glu	65	70	75	80
Gln	Leu	Ser	Glu	Gln	Gln	Ala	Leu	Ala	Leu	Ala	Gln	Glu	Arg	Ser	Asn	85	90	95	
Gly	Asn	Gly	His	Ser	Asn	Gly	Lys	Arg	His	Gln	Ser	Leu	Asp	Gly	Ala	100	105	110	
Met	Asn	Arg	Leu	Ser	Val	Gly	Ser	Asp	Ser	Ser	Ser	Ile	Gln	Gly	Ser	115	120	125	
Leu	Thr	Arg	Met	Ala	Thr	Asn	Ala	Ser	Thr	Ser	Ser	Leu	Ile	Ser	Gly	130	135	140	
Met	Pro	Asn	Asn	Asn	Thr	Leu	Phe	Thr	Phe	Thr	Ala	Gly	Val	Leu	Pro	145	150	155	160
Ala	Asn	Ile	Ser	Val	Asp	Pro	Ala	Thr	His	Leu	Trp	Lys	Leu	Phe	Gln	165	170	175	
Gln	Gly	Ala	Pro	Phe	Cys	Val	Leu	Ile	Asn	His	Ile	Leu	Pro	Asp	Ser	180	185	190	

Gln	Ile	Pro	Val	Val	Ser	Ser	Asp	Asp	Leu	Arg	Ile	Cys	Lys	Lys	Ser
		195					200					205			
Val	Tyr	Asp	Phe	Leu	Ile	Ala	Val	Lys	Thr	Gln	Leu	Asn	Phe	Asp	Asp
	210					215					220				
Glu	Asn	Met	Phe	Thr	Ile	Ser	Asn	Val	Phe	Ser	Asp	Asn	Ala	Gln	Asp
225					230					235					240
Leu	Ile	Lys	Ile	Ile	Asp	Val	Ile	Asn	Lys	Leu	Leu	Ala	Glu	Tyr	Ser
				245					250					255	
Asp	Ala	Ser	Asp	Ser	Gly	Gly	Gly	Asp	Glu	Asp	Val	Asn	Met	Asp	Val
			260					265					270		
Gln	Ile	Thr	Asp	Glu	Arg	Ser	Lys	Val	Phe	Arg	Glu	Ile	Ile	Glu	Thr
		275					280					285			
Glu	Arg	Lys	Tyr	Val	Gln	Asp	Leu	Glu	Leu	Met	Cys	Lys	Tyr	Arg	Gln
	290					295					300				
Asp	Leu	Ile	Glu	Ala	Glu	Asn	Leu	Ser	Ser	Glu	Gln	Ile	His	Leu	Leu
305					310					315					320
Phe	Pro	Asn	Leu	Asn	Glu	Ile	Ile	Asp	Phe	Gln	Arg	Arg	Phe	Leu	Asn
				325					330					335	
Gly	Leu	Glu	Cys	Asn	Ile	Asn	Val	Pro	Ile	Arg	Tyr	Gln	Arg	Ile	Gly
			340					345					350		
Ser	Val	Phe	Ile	His	Ala	Ser	Leu	Gly	Pro	Phe	Asn	Ala	Tyr	Glu	Pro
		355					360					365			
Trp	Thr	Ile	Gly	Gln	Leu	Thr	Ala	Ile	Asp	Leu	Ile	Asn	Lys	Glu	Ala
	370					375					380				
Ala	Asn	Leu	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Asp	Pro	Gly	Phe	Glu	Leu
385					390					395					400
Gln	Ser	Tyr	Ile	Leu	Lys	Pro	Ile	Gln	Arg	Leu	Cys	Lys	Tyr	Pro	Leu
				405					410					415	
Leu	Leu	Lys	Glu	Leu	Ile	Lys	Thr	Ser	Pro	Glu	Tyr	Ser	Lys	Gln	Asp
			420					425					430		
Pro	His	Gly	Ser	Ser	Ser	Ser	Thr	Ser	Phe	Asn	Glu	Leu	Leu	Val	Ala
		435					440					445			
Lys	Thr	Ala	Met	Lys	Glu	Leu	Ala	Asn	Gln	Val	Asn	Glu	Ala	Gln	Arg
		450				455					460				
Arg	Ala	Glu	Asn	Ile	Glu	His	Leu	Glu	Lys	Leu	Lys	Glu	Arg	Val	Gly
465					470					475					480
Asn	Trp	Arg	Gly	Phe	Asn	Leu	Asp	Ala	Gln	Gly	Glu	Leu	Leu	Phe	His
				485					490					495	
Gly	Gln	Val	Gly	Val	Lys	Asp	Ala	Glu	Asn	Glu	Lys	Glu	Tyr	Val	Ala
			500					505					510		

Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp Asp Thr  
 515 520 525  
 Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr Arg Lys  
 530 535 540  
 Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu Leu Glu  
 545 550 555 560  
 Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu Leu Lys  
 565 570 575  
 Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro Asn Thr  
 580 585 590  
 Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu Ser Gly  
 595 600 605  
 Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln Trp Glu  
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 Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln Ile His  
 625 630 635 640  
 Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp Ser Ala  
 645 650 655  
 Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln Ser Thr  
 660 665 670  
 Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg His His  
 675 680 685  
 Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val Lys Ser  
 690 695 700  
 Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp Ser Phe  
 705 710 715 720  
 Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser Leu Met  
 725 730 735  
 Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala Ile Lys  
 740 745 750  
 Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val Asn Ala  
 755 760 765  
 Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln Ile Ile  
 770 775 780  
 Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu Arg Tyr  
 785 790 795 800  
 Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp Asp Trp  
 805 810 815  
 Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp Phe Tyr Gln Thr Ser  
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 Ser Asn Glu Lys Arg Ser Val Thr Val Trp Val Ser



835

840

&lt;210&gt; 25

&lt;211&gt; 22

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 25

Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser  
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Ile Tyr Asp Phe Ile Leu  
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&lt;210&gt; 26

&lt;211&gt; 22

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 26

Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser  
 1 5 10 15

Val Tyr Asp Phe Leu Ile  
 20

&lt;210&gt; 27

&lt;211&gt; 854

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 27

Met Ala Ile Gln Thr Arg Phe Ala Ser Gly Thr Ser Leu Ser Asp Leu  
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Lys Pro Lys Pro Ser Ala Thr Ser Ile Ser Ile Pro Met Gln Asn Val  
 20 25 30

Met Asn Lys Pro Val Thr Glu Gln Asp Ser Leu Phe His Ile Cys Ala  
 35 40 45

Asn Ile Arg Lys Arg Leu Glu Val Leu Pro Gln Leu Lys Pro Phe Leu  
 50 55 60

Gln Leu Ala Tyr Gln Ser Ser Glu Val Leu Ser Glu Arg Gln Ser Leu  
 65 70 75 80

Leu Leu Ser Gln Lys Gln His Gln Glu Leu Leu Lys Ser Asn Gly Ala  
 85 90 95

Asn Arg Asp Ser Ser Asp Leu Ala Pro Thr Leu Arg Ser Ser Ile  
 100 105 110

Ser Thr Ala Thr Ser Leu Met Ser Met Glu Gly Ile Ser Tyr Thr Asn  
 115 120 125

Ser Asn Pro Ser Ala Thr Pro Asn Met Glu Asp Thr Leu Leu Thr Phe  
 130 135 140

Ser Met Gly Ile Leu Pro Ile Thr Met Asp Cys Asp Pro Val Thr Gln  
 145 150 155 160  
 Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu Cys Ile Leu Phe Asn  
 165 170 175  
 Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu  
 180 185 190  
 Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile Leu Gly Cys Lys Lys  
 195 200 205  
 His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr Ile Ser Asp Val Phe  
 210 215 220  
 Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu Glu Val Val Glu Thr  
 225 230 235 240  
 Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser Lys Ser Lys Thr Gln  
 245 250 255  
 Gln Ile Met Asn Ala Glu Asn Gln His Arg His Gln Pro Gln Gln Ser  
 260 265 270  
 Ser Lys Lys His Asn Glu Tyr Val Lys Ile Ile Lys Glu Phe Val Ala  
 275 280 285  
 Thr Glu Arg Lys Tyr Val His Asp Leu Glu Ile Leu Asp Lys Tyr Arg  
 290 295 300  
 Gln Gln Leu Leu Asp Ser Asn Leu Ile Thr Ser Glu Glu Leu Tyr Met  
 305 310 315 320  
 Leu Phe Pro Asn Leu Gly Asp Ala Ile Asp Phe Gln Arg Arg Phe Leu  
 325 330 335  
 Ile Ser Leu Glu Ile Asn Ala Leu Val Glu Pro Ser Lys Gln Arg Ile  
 340 345 350  
 Gly Ala Leu Phe Met His Ser Lys His Phe Phe Lys Leu Tyr Glu Pro  
 355 360 365  
 Trp Ser Ile Gly Gln Asn Ala Ala Ile Glu Phe Leu Ser Ser Thr Leu  
 370 375 380  
 His Lys Met Arg Val Asp Glu Ser Gln Arg Phe Ile Ile Asn Asn Lys  
 385 390 395 400  
 Leu Glu Leu Gln Ser Phe Leu Tyr Lys Pro Val Gln Arg Leu Cys Arg  
 405 410 415  
 Tyr Pro Leu Leu Val Lys Glu Leu Leu Ala Glu Ser Ser Asp Asp Asn  
 420 425 430  
 Asn Thr Lys Glu Leu Glu Ala Ala Leu Asp Ile Ser Lys Asn Ile Ala  
 435 440 445  
 Arg Ser Ile Asn Glu Asn Gln Arg Arg Thr Glu Asn His Gln Val Val  
 450 455 460

Lys Lys Leu Tyr Gly Arg Val Val Asn Trp Lys Gly Tyr Arg Ile Ser  
 465 470 475 480  
 Lys Phe Gly Glu Leu Leu Tyr Phe Asp Lys Val Phe Ile Ser Thr Thr  
 485 490 495  
 Asn Ser Ser Ser Glu Pro Glu Arg Glu Phe Glu Val Tyr Leu Phe Glu  
 500 505 510  
 Lys Ile Ile Ile Leu Phe Ser Glu Val Val Thr Lys Lys Ser Ala Ser  
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 Ser Leu Ile Leu Lys Lys Lys Ser Ser Thr Ser Ala Ser Ile Ser Ala  
 530 535 540  
 Ser Asn Ile Thr Asp Asn Asn Gly Ser Pro His His Ser Tyr His Lys  
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 Arg His Ser Asn Ser Ser Ser Ser Asn Asn Ile His Leu Ser Ser Ser  
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 580 585 590  
 Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys Leu Ser Ala Asn Glu  
 595 600 605  
 Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile Met Asn Leu Asn Gln  
 610 615 620  
 Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile Thr Trp Glu Ser Ile  
 625 630 635 640  
 Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys Asn Glu Glu Thr Arg  
 645 650 655  
 Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile His Asp Leu Lys Asn  
 660 665 670  
 Glu Gln Phe Lys Ala Arg His His Ser Ser Thr Ser Thr Thr Ser Ser  
 675 680 685  
 Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr Thr Thr Met Asn Thr  
 690 695 700  
 Pro Asn His His Asn Ser Arg Gln Thr His Asp Ser Met Ala Ser Phe  
 705 710 715 720  
 Ser Ser Ser His Met Lys Arg Val Ser Asp Val Leu Pro Lys Arg Arg  
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 Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys Ser Ile Ser Glu Asn  
 740 745 750  
 Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu Phe Arg Ile Ser Tyr  
 755 760 765  
 Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu Ile Phe Thr Leu Leu  
 770 775 780  
 Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile Met Ala Ile Asn Ser

785						790						795						800
Lys	Ile	Ser	Asn	Thr	His	Asn	Asn	Asn	Ile	Ser	Pro	Ile	Thr	Lys	Ile			
				805					810					815				
Lys	Tyr	Gln	Asp	Glu	Asp	Gly	Asp	Phe	Val	Val	Leu	Gly	Ser	Asp	Glu			
				820					825					830				
Asp	Trp	Asn	Val	Ala	Lys	Glu	Met	Leu	Ala	Glu	Asn	Asn	Glu	Lys	Phe			
				835					840					845				
Leu	Asn	Ile	Arg	Leu	Tyr													
		850																

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<210> 28
<211> 837
<212> PRT
<213> Saccharomyces cerevisiae
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<400>	28															
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Ile	Ser	Ile	Pro	Met	Gln	Asn	Val	Met	Asn	Lys	Pro	Val	Thr	Glu	Gln	
			20					25					30			
Asp	Ser	Leu	Phe	His	Ile	Cys	Ala	Asn	Ile	Arg	Lys	Arg	Leu	Glu	Val	
		35					40					45				
Leu	Pro	Gln	Leu	Lys	Pro	Phe	Leu	Gln	Leu	Ala	Tyr	Gln	Ser	Ser	Glu	
	50					55					60					
Val	Leu	Ser	Glu	Arg	Gln	Ser	Leu	Leu	Leu	Ser	Gln	Lys	Gln	His	Gln	
65					70					75					80	
Glu	Leu	Leu	Lys	Ser	Asn	Gly	Ala	Asn	Arg	Asp	Ser	Ser	Asp	Leu	Ala	
				85					90					95		
Pro	Thr	Leu	Arg	Ser	Ser	Ser	Ile	Ser	Thr	Ala	Thr	Ser	Leu	Met	Ser	
			100					105					110			
Met	Glu	Gly	Ile	Ser	Tyr	Thr	Asn	Ser	Asn	Pro	Ser	Ala	Thr	Pro	Asn	
		115					120					125				
Met	Glu	Asp	Thr	Leu	Leu	Thr	Phe	Ser	Met	Gly	Ile	Leu	Pro	Ile	Thr	
	130					135					140					
Met	Asp	Cys	Asp	Pro	Val	Thr	Gln	Leu	Ser	Gln	Leu	Phe	Gln	Gln	Gly	
145					150					155					160	
Ala	Pro	Leu	Cys	Ile	Leu	Phe	Asn	Ser	Val	Lys	Pro	Gln	Phe	Lys	Leu	
				165					170					175		
Pro	Val	Ile	Ala	Ser	Asp	Asp	Leu	Lys	Val	Cys	Lys	Lys	Ser	Ile	Tyr	
			180					185					190			
Asp	Phe	Ile	Leu	Gly	Cys	Lys	Lys	His	Phe	Ala	Phe	Asn	Asp	Glu	Glu	
		195					200					205				
Leu	Phe	Thr	Ile	Ser	Asp	Val	Phe	Ala	Asn	Ser	Thr	Ser	Gln	Leu	Val	

210	215	220
Lys Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile 225 230 235 240		
Phe Pro Ser Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln 245 250 255		
His Arg His Gln Pro Gln Gln Ser Ser Lys Lys His Asn Glu Tyr Val 260 265 270		
Lys Ile Ile Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp 275 280 285		
Leu Glu Ile Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu 290 295 300		
Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala 305 310 315 320		
Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu 325 330 335		
Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys 340 345 350		
His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala 355 360 365		
Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser 370 375 380		
Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr 385 390 395 400		
Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu 405 410 415		
Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala 420 425 430		
Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg 435 440 445		
Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val 450 455 460		
Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe 465 470 475 480		
Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg 485 490 495		
Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu 500 505 510		
Val Val Thr Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser 515 520 525		
Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly 530 535 540		

Ser Pro His His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Ser  
 545 550 555 560  
 Asn Asn Ile His Leu Ser Ser Ser Ser Ala Ala Ala Ile Ile His Ser  
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 Ser Thr Asn Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser  
 580 585 590  
 Leu Phe Lys Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg  
 595 600 605  
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 610 615 620  
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 625 630 635 640  
 Lys Phe Lys Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln  
 645 650 655  
 Gln Leu Ile His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His  
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 Ser Ser Thr Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met  
 675 680 685  
 Ser Pro Thr Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln  
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 Thr His Asp Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val  
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 740 745 750  
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 Ser Ser Glu Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp  
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 Asp Leu Ile Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn  
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 Asn Ile Ser Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp  
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 Leu Ala Glu Asn Asn  
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<210> 29  
 <211> 813

<212> PRT

<213> Candida albicans

<400> 29

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Val Ser Ser Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr  
20 25 30

Pro Lys Asp His Leu Phe Tyr Arg Cys Glu Ser Leu Lys Arg Lys Leu  
35 40 45

Gln Lys Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln  
50 55 60

Ala Glu Gln Leu Ser Glu Gln Gln Ala Leu Ala Leu Ala Gln Glu Arg  
65 70 75 80

Ser Asn Gly Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp  
85 90 95

Gly Ala Met Asn Arg Leu Ser Val Gly Ser Asp Ser Ser Ser Ile Gln  
100 105 110

Gly Ser Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile  
115 120 125

Ser Gly Met Pro Asn Asn Asn Thr Leu Phe Thr Phe Thr Ala Gly Val  
130 135 140

Leu Pro Ala Asn Ile Ser Val Asp Pro Ala Thr His Leu Trp Lys Leu  
145 150 155 160

Phe Gln Gln Gly Ala Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro  
165 170 175

Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys  
180 185 190

Lys Ser Val Tyr Asp Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe  
195 200 205

Asp Asp Glu Asn Met Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala  
210 215 220

Gln Asp Leu Ile Lys Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu  
225 230 235 240

Tyr Ser Asp Ala Ser Asp Ser Gly Gly Gly Asp Glu Asp Val Asn Met  
245 250 255

Asp Val Gln Ile Thr Asp Glu Arg Ser Lys Val Phe Arg Glu Ile Ile  
260 265 270

Glu Thr Glu Arg Lys Tyr Val Gln Asp Leu Glu Leu Met Cys Lys Tyr  
275 280 285

Arg Gln Asp Leu Ile Glu Ala Glu Asn Leu Ser Ser Glu Gln Ile His  
290 295 300

Leu Leu Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe  
 305 310 315 320  
 Leu Asn Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg  
 325 330 335  
 Ile Gly Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr  
 340 345 350  
 Glu Pro Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys  
 355 360 365  
 Glu Ala Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe  
 370 375 380  
 Glu Leu Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr  
 385 390 395 400  
 Pro Leu Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys  
 405 410 415  
 Gln Asp Pro His Gly Ser Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu  
 420 425 430  
 Val Ala Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala  
 435 440 445  
 Gln Arg Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg  
 450 455 460  
 Val Gly Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu  
 465 470 475 480  
 Phe His Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr  
 485 490 495  
 Val Ala Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp  
 500 505 510  
 Asp Thr Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr  
 515 520 525  
 Arg Lys Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu  
 530 535 540  
 Leu Glu Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu  
 545 550 555 560  
 Leu Lys Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro  
 565 570 575  
 Asn Thr Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu  
 580 585 590  
 Ser Gly Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln  
 595 600 605  
 Trp Glu Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln  
 610 615 620  
 Ile His Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp



625		630		635		640
Ser Ala Ile Tyr Asp	Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln					
645		650		655		
Ser Thr Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg						
660	665	670				
His His Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val						
675	680	685				
Lys Ser Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp						
690	695	700				
Ser Phe Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser						
705	710	715		720		
Leu Met Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala						
725	730	735				
Ile Lys Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val						
740	745	750				
Asn Ala Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln						
755	760	765				
Ile Ile Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu						
770	775	780				
Arg Tyr Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp						
785	790	795		800		
Asp Trp Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp						
805	810					

<210> 30  
 <211> 684  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 30
Asp Pro Val Thr Gln Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu
1 5 10 15
Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile
20 25 30
Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile
35 40 45
Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr
50 55 60
Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu
65 70 75 80
Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser
85 90 95
Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln His Arg His

100										105					110						
Gln	Pro	Gln	Gln	Ser	Ser	Lys	Lys	His	Asn	Glu	Tyr	Val	Lys	Ile	Ile						
		115					120					125									
Lys	Glu	Phe	Val	Ala	Thr	Glu	Arg	Lys	Tyr	Val	His	Asp	Leu	Glu	Ile						
	130					135					140										
Leu	Asp	Lys	Tyr	Arg	Gln	Gln	Leu	Leu	Asp	Ser	Asn	Leu	Ile	Thr	Ser						
145					150					155					160						
Glu	Glu	Leu	Tyr	Met	Leu	Phe	Pro	Asn	Leu	Gly	Asp	Ala	Ile	Asp	Phe						
				165					170					175							
Gln	Arg	Arg	Phe	Leu	Ile	Ser	Leu	Glu	Ile	Asn	Ala	Leu	Val	Glu	Pro						
			180					185					190								
Ser	Lys	Gln	Arg	Ile	Gly	Ala	Leu	Phe	Met	His	Ser	Lys	His	Phe	Phe						
		195					200					205									
Lys	Leu	Tyr	Glu	Pro	Trp	Ser	Ile	Gly	Gln	Asn	Ala	Ala	Ile	Glu	Phe						
	210					215					220										
Leu	Ser	Ser	Thr	Leu	His	Lys	Met	Arg	Val	Asp	Glu	Ser	Gln	Arg	Phe						
225					230					235					240						
Ile	Ile	Asn	Asn	Lys	Leu	Glu	Leu	Gln	Ser	Phe	Leu	Tyr	Lys	Pro	Val						
				245					250					255							
Gln	Arg	Leu	Cys	Arg	Tyr	Pro	Leu	Leu	Val	Lys	Glu	Leu	Leu	Ala	Glu						
			260					265					270								
Ser	Ser	Asp	Asp	Asn	Asn	Thr	Lys	Glu	Leu	Glu	Ala	Ala	Leu	Asp	Ile						
		275					280					285									
Ser	Lys	Asn	Ile	Ala	Arg	Ser	Ile	Asn	Glu	Asn	Gln	Arg	Arg	Thr	Glu						
	290					295					300										
Asn	His	Gln	Val	Val	Lys	Lys	Leu	Tyr	Gly	Arg	Val	Val	Asn	Trp	Lys						
305					310					315					320						
Gly	Tyr	Arg	Ile	Ser	Lys	Phe	Gly	Glu	Leu	Leu	Tyr	Phe	Asp	Lys	Val						
				325					330					335							
Phe	Ile	Ser	Thr	Thr	Asn	Ser	Ser	Ser	Glu	Pro	Glu	Arg	Glu	Phe	Glu						
			340					345					350								
Val	Tyr	Leu	Phe	Glu	Lys	Ile	Ile	Ile	Leu	Phe	Ser	Glu	Val	Val	Thr						
		355					360					365									
Lys	Lys	Ser	Ala	Ser	Ser	Leu	Ile	Leu	Lys	Lys	Lys	Ser	Ser	Thr	Ser						
	370	</																			

Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys  
 435 440 445  
 Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile  
 450 455 460  
 Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile  
 465 470 475 480  
 Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys  
 485 490 495  
 Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile  
 500 505 510  
 His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His Ser Ser Thr  
 515 520 525  
 Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr  
 530 535 540  
 Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln Thr His Asp  
 545 550 555 560  
 Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val Ser Asp Val  
 565 570 575  
 Leu Pro Lys Arg Arg Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys  
 580 585 590  
 Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu  
 595 600 605  
 Phe Arg Ile Ser Tyr Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu  
 610 615 620  
 Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile  
 625 630 635 640  
 Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn Asn Ile Ser  
 645 650 655  
 Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp Phe Val Val  
 660 665 670  
 Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu  
 675 680

<210> 31  
 <211> 742  
 <212> PRT  
 <213> Schizosaccharomyces pombe

<400> 31  
 Asp Pro Val Thr Glu Ile Trp Leu Phe Cys Arg Leu Gly Tyr Pro Leu  
 1 5 10 15  
 Cys Ala Leu Phe Asn Cys Leu Pro Val Lys Gln Lys Leu Glu Val Asn  
 20 25 30

Ser Ser Val Ser Leu Glu Asn Thr Asn Val Cys Lys Ala Ser Leu Tyr  
 35 40 45  
 Arg Phe Met Leu Met Cys Lys Asn Glu Leu Gly Leu Thr Asp Ala Ala  
 50 55 60  
 Leu Phe Ser Ile Ser Glu Ile Tyr Lys Pro Ser Thr Ala Pro Leu Val  
 65 70 75 80  
 Arg Ala Leu Gln Thr Ile Glu Leu Leu Leu Lys Lys Tyr Glu Val Ser  
 85 90 95  
 Asn Thr Thr Lys Ser Ser Ser Thr Pro Ser Pro Ser Thr Asp Asp Asn  
 100 105 110  
 Val Pro Thr Gly Thr Leu Asn Ser Leu Ile Ala Ser Gly Arg Arg Val  
 115 120 125  
 Thr Ala Glu Leu Tyr Glu Thr Glu Leu Lys Tyr Ile Gln Asp Leu Glu  
 130 135 140  
 Tyr Leu Ser Asn Tyr Met Val Ile Leu Gln Gln Lys Gln Ile Leu Ser  
 145 150 155 160  
 Gln Asp Thr Ile Leu Ser Ile Phe Thr Asn Leu Asn Glu Ile Leu Asp  
 165 170 175  
 Phe Gln Arg Arg Phe Leu Val Gly Leu Glu Met Asn Leu Ser Leu Pro  
 180 185 190  
 Val Glu Glu Gln Arg Leu Gly Ala Leu Phe Ile Ala Leu Glu Glu Gly  
 195 200 205  
 Phe Ser Val Tyr Gln Val Phe Cys Thr Asn Phe Pro Asn Ala Gln Gln  
 210 215 220  
 Leu Ile Ile Asp Asn Gln Asn Gln Leu Leu Lys Val Ala Asn Leu Leu  
 225 230 235 240  
 Glu Pro Ser Tyr Glu Leu Pro Ala Leu Leu Ile Lys Pro Ile Gln Arg  
 245 250 255  
 Ile Cys Lys Tyr Pro Leu Leu Leu Asn Gln Leu Leu Lys Gly Thr Pro  
 260 265 270  
 Ser Gly Tyr Gln Tyr Glu Glu Glu Leu Lys Gln Gly Met Ala Cys Val  
 275 280 285  
 Val Arg Val Ala Asn Gln Val Asn Glu Thr Arg Arg Ile His Glu Asn  
 290 295 300  
 Arg Asn Ala Ile Ile Glu Leu Glu Gln Arg Val Ile Asp Trp Lys Gly  
 305 310 315 320  
 Tyr Ser Leu Gln Tyr Phe Gly Gln Leu Leu Val Trp Asp Val Val Asn  
 325 330 335  
 Val Cys Lys Ala Asp Ile Glu Arg Glu Tyr His Val Tyr Leu Phe Glu  
 340 345 350

Lys Ile Leu Leu Cys Cys Lys Glu Met Ser Thr Leu Lys Arg Gln Ala  
 355 360 365  
 Arg Ser Ile Ser Met Asn Lys Lys Thr Lys Arg Leu Asp Ser Leu Gln  
 370 375 380  
 Leu Lys Gly Arg Ile Leu Thr Ser Asn Ile Thr Thr Val Val Pro Asn  
 385 390 395 400  
 His His Met Gly Ser Tyr Ala Ile Gln Ile Phe Trp Arg Gly Asp Pro  
 405 410 415  
 Gln His Glu Ser Phe Ile Leu Lys Leu Arg Asn Glu Glu Ser His Lys  
 420 425 430  
 Leu Trp Met Ser Val Leu Asn Arg Leu Leu Trp Lys Asn Glu His Gly  
 435 440 445  
 Ser Pro Lys Asp Ile Arg Ser Ala Ala Ser Thr Pro Ala Asn Pro Val  
 450 455 460  
 Tyr Asn Arg Ser Ser Ser Gln Thr Ser Lys Gly Tyr Asn Ser Ser Asp  
 465 470 475 480  
 Tyr Asp Leu Leu Arg Thr His Ser Leu Asp Glu Asn Val Asn Ser Pro  
 485 490 495  
 Thr Ser Ile Ser Ser Pro Ser Ser Lys Ser Ser Pro Phe Thr Lys Thr  
 500 505 510  
 Thr Ser Lys Asp Thr Lys Ser Ala Thr Thr Thr Asp Glu Arg Pro Ser  
 515 520 525  
 Asp Phe Ile Arg Leu Asn Ser Glu Glu Ser Val Gly Thr Ser Ser Leu  
 530 535 540  
 Arg Thr Ser Gln Thr Thr Ser Thr Ile Val Ser Asn Asp Ser Ser Ser  
 545 550 555 560  
 Thr Ala Ser Ile Pro Ser Gln Ile Ser Arg Ile Ser Gln Val Asn Ser  
 565 570 575  
 Leu Leu Asn Asp Tyr Asn Tyr Asn Arg Gln Ser His Ile Thr Arg Val  
 580 585 590  
 Tyr Ser Gly Thr Asp Asp Gly Ser Ser Val Ser Ile Phe Glu Asp Thr  
 595 600 605  
 Ser Ser Ser Thr Lys Gln Lys Ile Phe Asp Gln Pro Thr Thr Asn Asp  
 610 615 620  
 Cys Asp Val Met Arg Pro Arg Gln Tyr Ser Tyr Ser Ala Gly Met Lys  
 625 630 635 640  
 Ser Asp Gly Ser Leu Leu Pro Ser Thr Lys His Thr Ser Leu Ser Ser  
 645 650 655  
 Ser Ser Thr Ser Thr Ser Leu Ser Val Arg Asn Thr Thr Asn Val Lys  
 660 665 670  
 Ile Arg Leu Arg Leu His Glu Val Ser Leu Val Leu Val Val Ala His



35                      40                      45  
 Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys  
     50                      55                      60  
 Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr  
 65                      70                      75  
 <210> 35 <211> 19 <212> PRT <213> Candida albicans <400> 35  
 Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys  
 1                      5                      10                      15  
 Lys Ser Val  
  
 <210> 36  
 <211> 73  
 <212> PRT  
 <213> Candida albicans  
  
 <400> 36  
 Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro  
 1                      5                      10                      15  
 Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp  
                     20                      25                      30  
 Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met  
                     35                      40                      45  
 Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys  
                     50                      55                      60  
 Ile Ile Asp Val Ile Asn Lys Leu Leu  
 65                      70  
 <210> 37  
 <211> 73  
 <212> PRT  
 <213> Saccharomyces cerevisiae  
  
 <400> 37  
 Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro  
 1                      5                      10                      15  
 Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp  
                     20                      25                      30  
 Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu  
                     35                      40                      45  
 Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys  
                     50                      55                      60  
 Val Leu Glu Val Val Glu Thr Leu Met  
 65                      70